



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 08:04 PM UTC

PDB ID : 7OHP / pdb_00007ohp
EMDB ID : EMD-12904
Title : Nog1-TAP associated immature ribosomal particles from *S. cerevisiae* after rpL25 expression shut down, population A
Authors : Milkereit, P.; Poell, G.
Deposited on : 2021-05-11
Resolution : 3.90 Å(reported)
Based on initial model : 6EM1

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

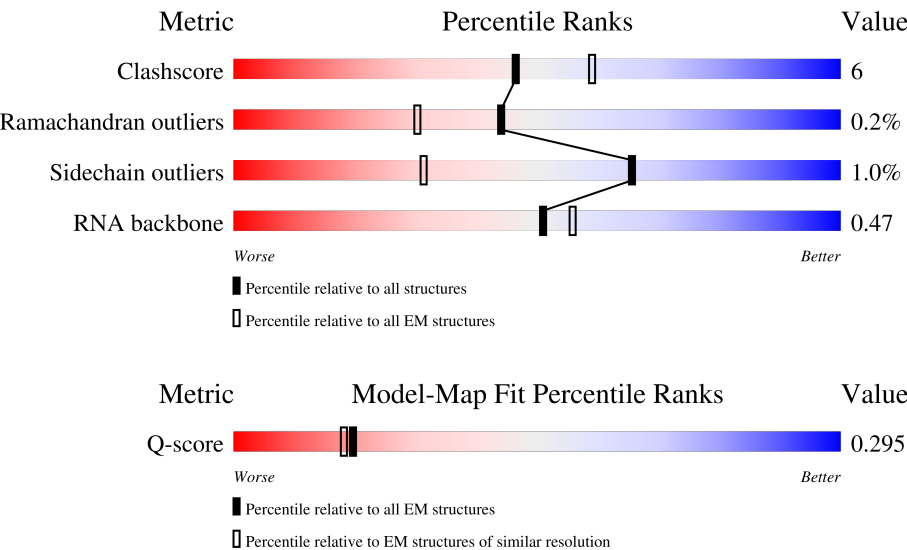
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8855 (3.40 - 4.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1	3396	27%15%5%54%
2	2	158	53%33%9%6%
3	6	232	12%10%6%72%

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Mol	Chain	Length	Quality of chain
4	B	387	
5	C	362	
6	D	505	
7	E	176	
8	F	244	
9	G	256	
10	H	191	
11	K	376	
12	L	199	
13	M	138	
14	N	204	
15	O	199	
16	P	184	
17	Q	186	
18	S	172	
19	V	137	
20	W	236	
21	Y	127	
22	b	647	
23	e	130	
24	f	107	
25	h	120	
26	i	100	
27	j	88	
28	m	807	

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Mol	Chain	Length	Quality of chain
29	n	605	
30	o	220	
31	r	261	
32	t	322	
33	v	231	
34	y	245	

2 Entry composition

There are 35 unique types of molecules in this entry. The entry contains 143939 atoms, of which 63394 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	1	1567	Total	C	H	N	O	P	0	0
			50411	14981	16855	6074	10934	1567		

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	2	149	Total	C	H	N	O	P	0	0
			4764	1415	1601	556	1043	149		

- Molecule 3 is a RNA chain called ITS2.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	6	65	Total	C	H	N	O	P	0	0
			2061	614	691	228	463	65		

- Molecule 4 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	B	333	Total	C	H	N	O	S	0	0
			5374	1680	2728	490	470	6		

- Molecule 5 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	C	320	Total	C	H	N	O	S	0	0
			5071	1565	2597	469	437	3		

- Molecule 6 is a protein called ATP-dependent RNA helicase HAS1.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	D	167	Total	C	H	N	O	S	0	0
			2769	900	1384	229	251	5		

- Molecule 7 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	E	140	Total	C	H	N	O	S	0	0
			2328	721	1212	202	192	1		

- Molecule 8 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	F	222	Total	C	H	N	O	S	0	0
			3647	1151	1863	324	308	1		

- Molecule 9 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	G	155	Total	C	H	N	O	S	0	0
			2459	776	1261	202	218	2		

- Molecule 10 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	H	181	Total	C	H	N	O	S	0	0
			2955	917	1513	262	259	4		

- Molecule 11 is a protein called Proteasome-interacting protein CIC1.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	K	239	Total	C	H	N	O	S	0	0
			3954	1250	2026	321	354	3		

- Molecule 12 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	108	Total	C	H	N	O	0	0
			1782	541	918	180	143		

- Molecule 13 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	M	126	Total	C	H	N	O	S	0	0
			2064	634	1080	187	161	2		

- Molecule 14 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	N	158	Total	C	H	N	O	S	0	0
			2733	846	1388	280	218	1		

- Molecule 15 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	O	194	Total	C	H	N	O	S	0	0
			3171	987	1640	285	258	1		

- Molecule 16 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	P	98	Total	C	H	N	O	S	0	0
			1524	478	767	135	144			

- Molecule 17 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	Q	125	Total	C	H	N	O	S	0	0
			2000	615	1040	178	166	1		

- Molecule 18 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	S	163	Total	C	H	N	O	S	0	0
			2805	890	1425	258	229	3		

- Molecule 19 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	V	126	Total	C	H	N	O	S	0	0
			1923	588	987	176	165	7		

- Molecule 20 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	W	217	Total	C	H	N	O	S	0	0
			3547	1116	1787	304	336	4		

- Molecule 21 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Y	125	Total	C	H	N	O	0	0
			2060	620	1076	191	173		

- Molecule 22 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	b	394	Total	C	H	N	O	S	0	0
			6407	2037	3221	540	591	18		

- Molecule 23 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace	
23	e	118	Total	C	H	N	O	S	0	0
			1990	611	1029	195	154	1		

- Molecule 24 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	f	106	Total	C	H	N	O	S	0	0
			1731	540	881	165	144	1		

- Molecule 25 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
25	h	111	Total	C	H	N	O	S	0	0
			1911	575	1006	173	156	1		

- Molecule 26 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	i	74	Total	C	H	N	O	S	0	0
			1236	367	642	125	101	1		

- Molecule 27 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	j	71	Total	C	H	N	O	S	0	0
			1137	344	571	123	94	5		

- Molecule 28 is a protein called Ribosome biogenesis protein ERB1.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	m	142	Total	C	H	N	O	S	0	0
			2415	775	1208	212	217	3		

- Molecule 29 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	n	314	Total	C	H	N	O	S	0	0
			5222	1697	2642	428	447	8		

- Molecule 30 is a protein called Ribosome biogenesis protein 15.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	o	118	Total	C	H	N	O	S	0	0
			2009	632	1026	178	169	4		

- Molecule 31 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	r	73	Total	C	H	N	O	S	0	0
			1288	388	660	133	106	1		

- Molecule 32 is a protein called Ribosome biogenesis protein RLP7.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	t	226	Total	C	H	N	O	S	0	0
			3684	1144	1895	320	322	3		

- Molecule 33 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	v	121	Total	C	H	N	O	S	0	0
			2108	645	1077	201	182	3		

- Molecule 34 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	y	225	Total	C	H	N	O	S	0	0
			3398	1056	1697	295	343	7		

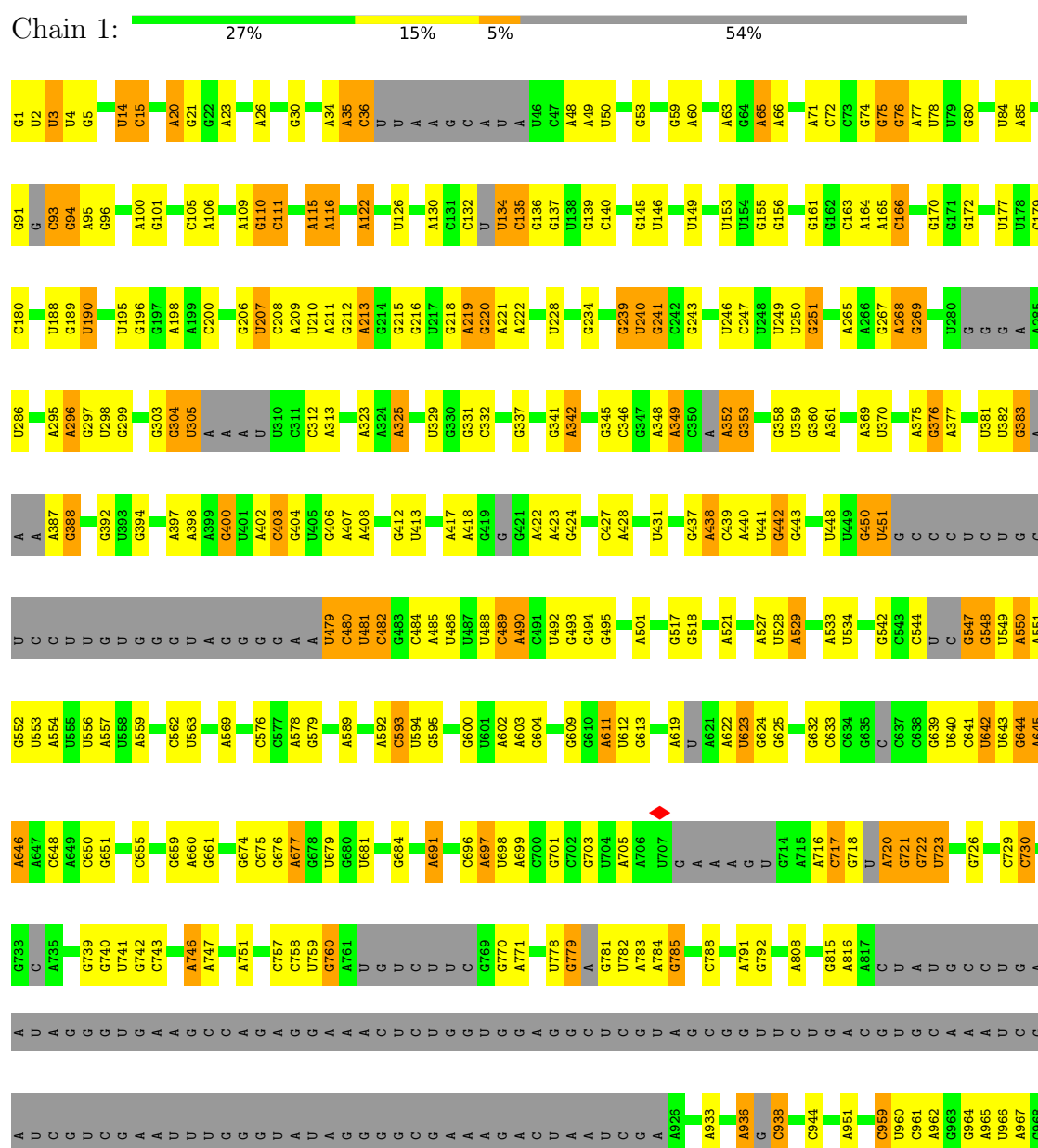
- Molecule 35 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
35	j	1	Total	Zn	0
			1	1	

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

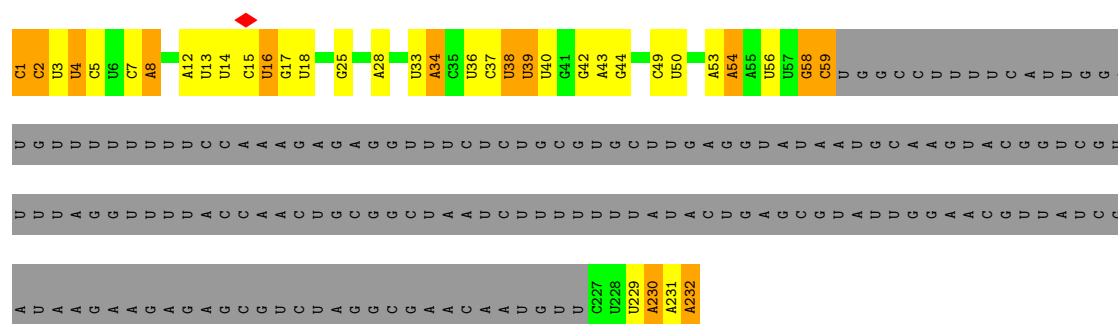
• Molecule 1: 25S rRNA





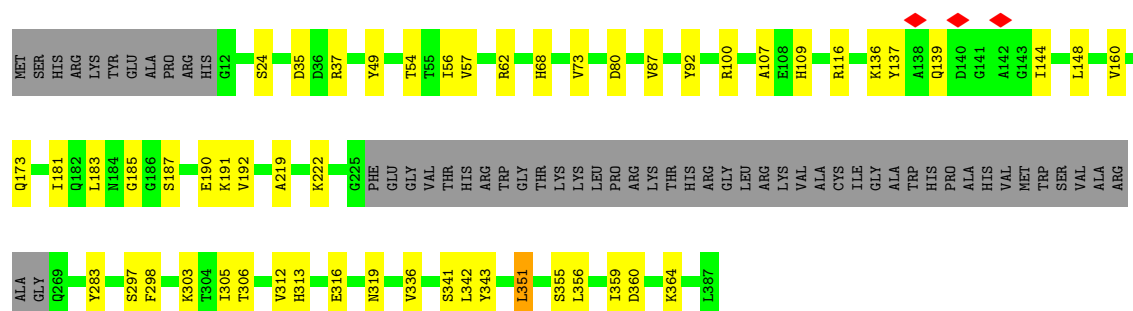
- Molecule 3: ITS2

Chain 6: 



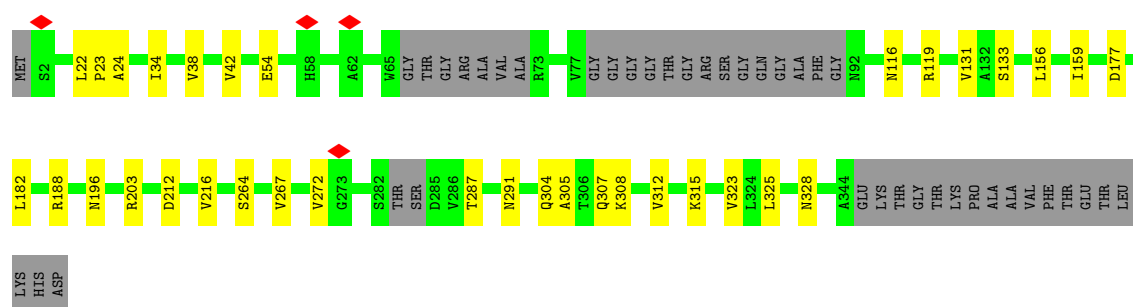
- Molecule 4: 60S ribosomal protein L3

Chain B: 



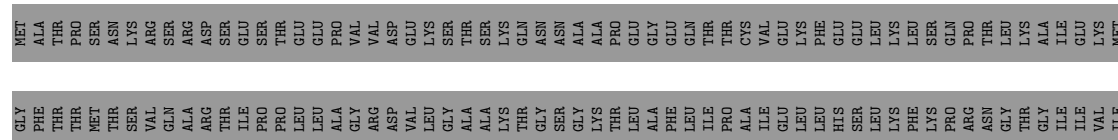
- Molecule 5: 60S ribosomal protein L4-A

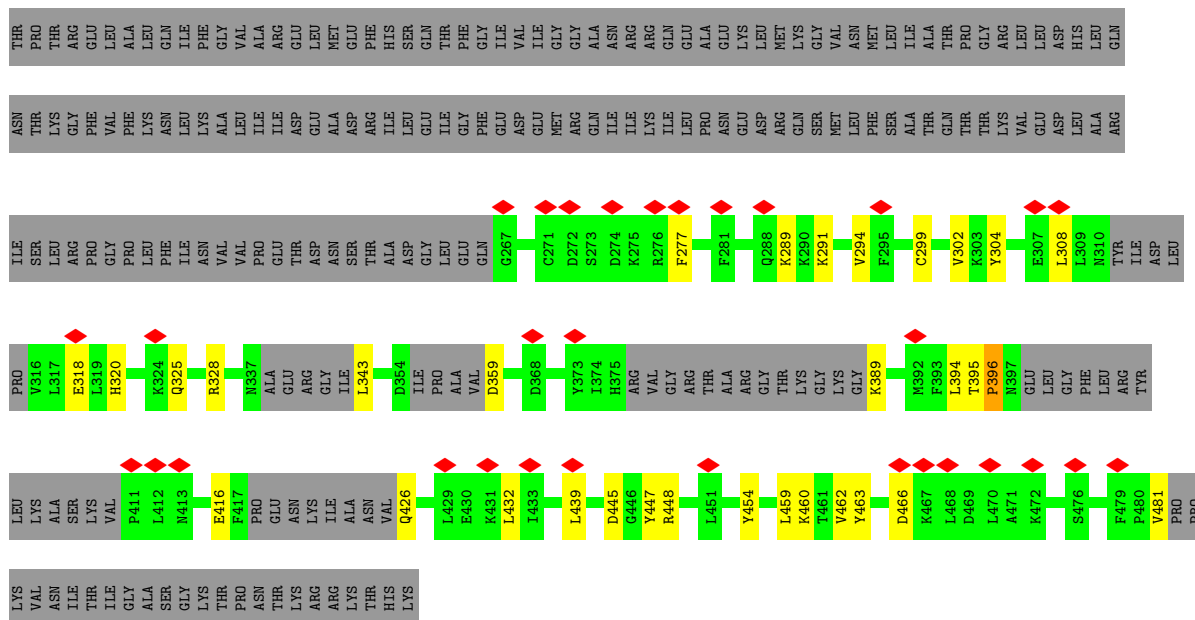
Chain C: 



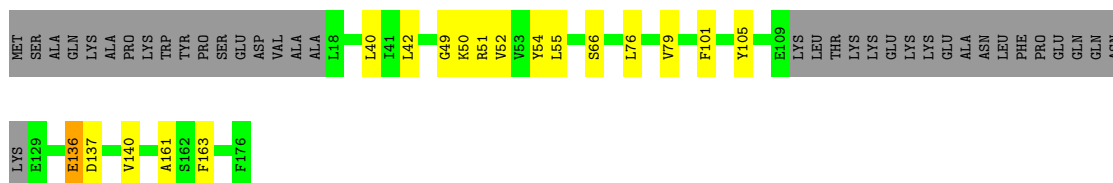
- Molecule 6: ATP-dependent RNA helicase HAS1

Chain D: 

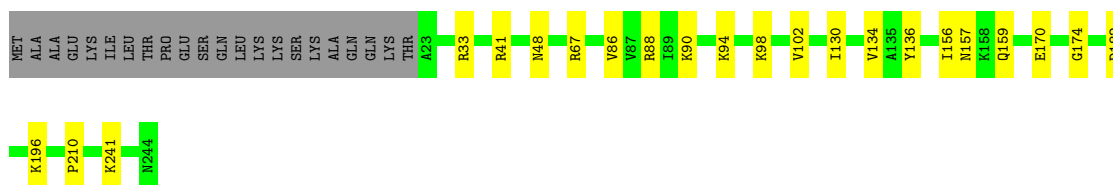
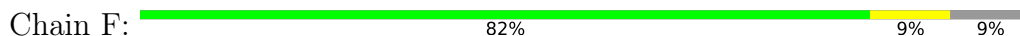




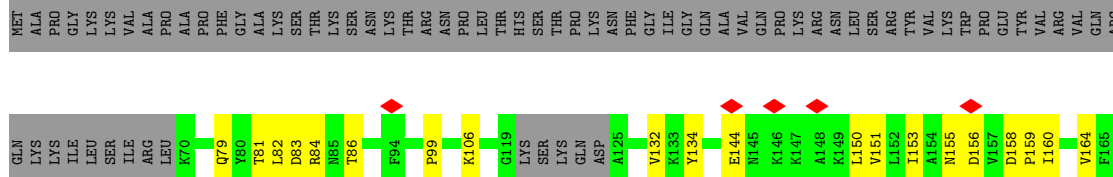
- Molecule 7: 60S ribosomal protein L6-A

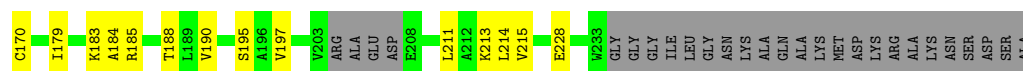


- Molecule 8: 60S ribosomal protein L7-A

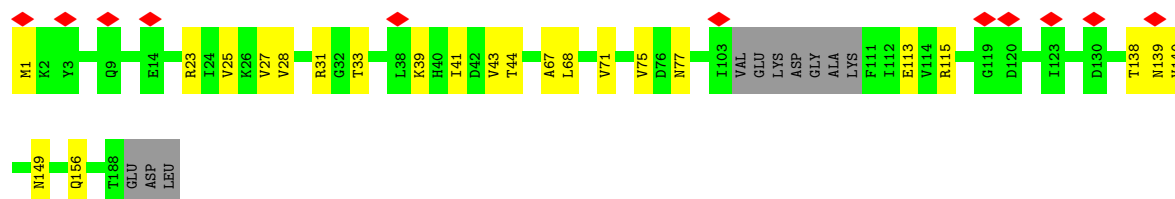
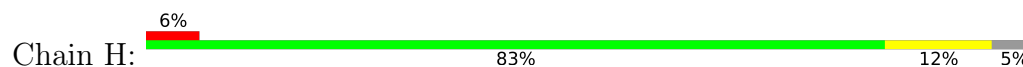


- Molecule 9: 60S ribosomal protein L8-A

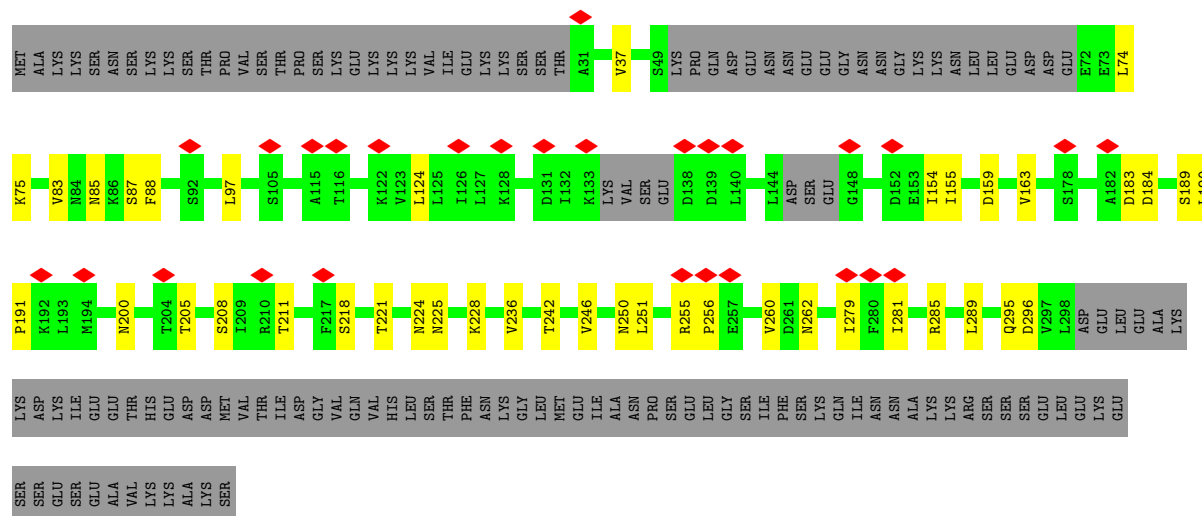




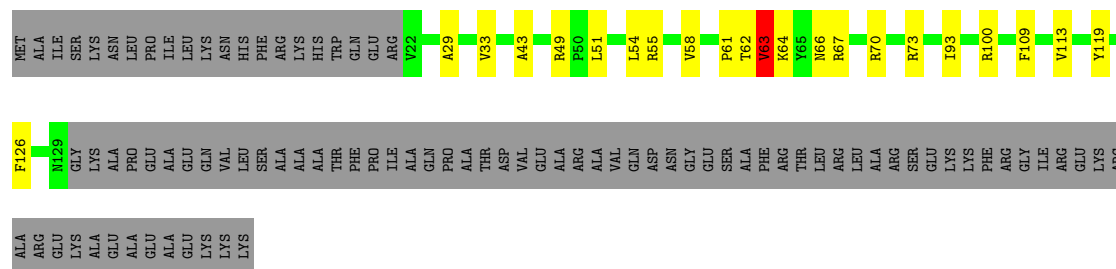
- Molecule 10: 60S ribosomal protein L9-A



- Molecule 11: Proteasome-interacting protein CIC1

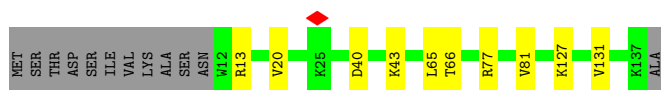


- Molecule 12: 60S ribosomal protein L13-A



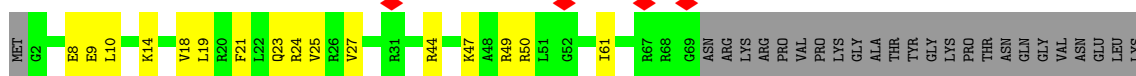
- Molecule 13: 60S ribosomal protein L14-A





• Molecule 14: 60S ribosomal protein L15-A

Chain N: 64% 13% 23%



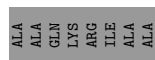
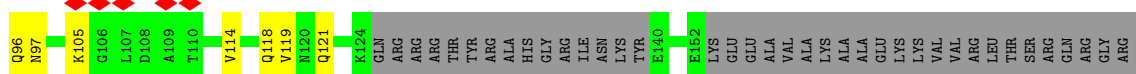
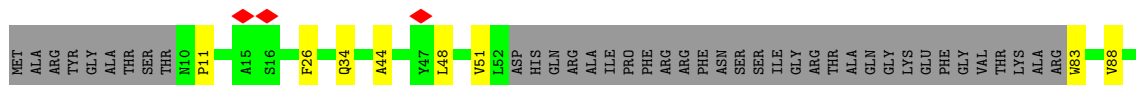
• Molecule 15: 60S ribosomal protein L16-A

Chain O: 93% 5%



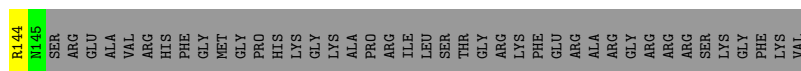
• Molecule 16: 60S ribosomal protein L17-A

Chain P: 45% 8% 47%



• Molecule 17: 60S ribosomal protein L18-A

Chain Q: 55% 12% 33%



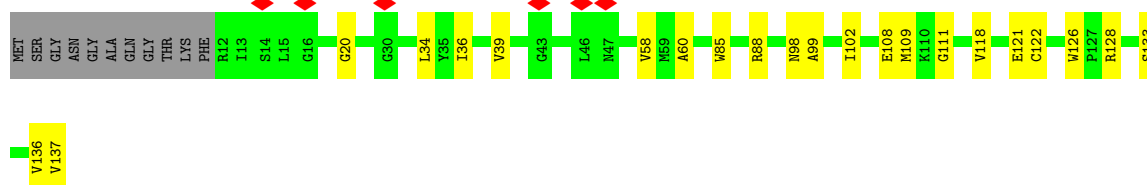
• Molecule 18: 60S ribosomal protein L20-A

Chain S: 84% 10% 5%



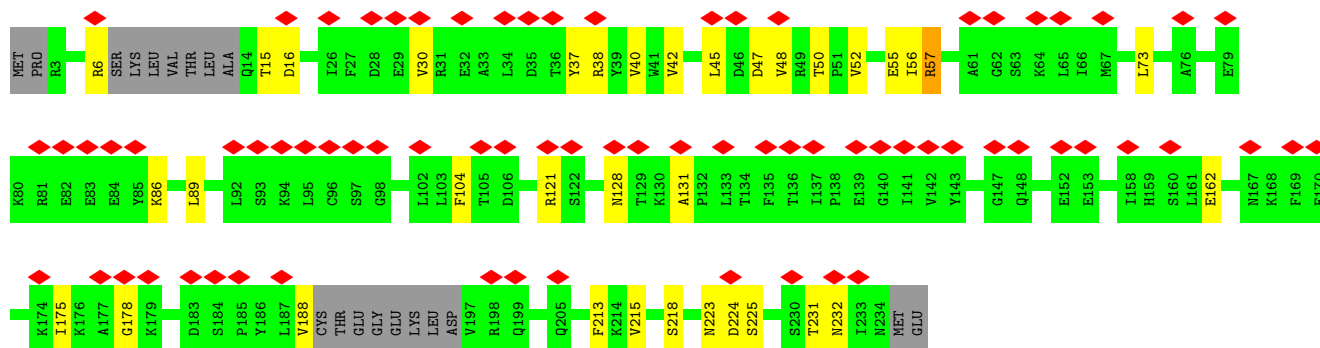
- Molecule 19: 60S ribosomal protein L23-A

Chain V: 76% 16% 8%



- Molecule 20: Ribosome assembly factor MRT4

Chain W: 31% 77% 14% 8%



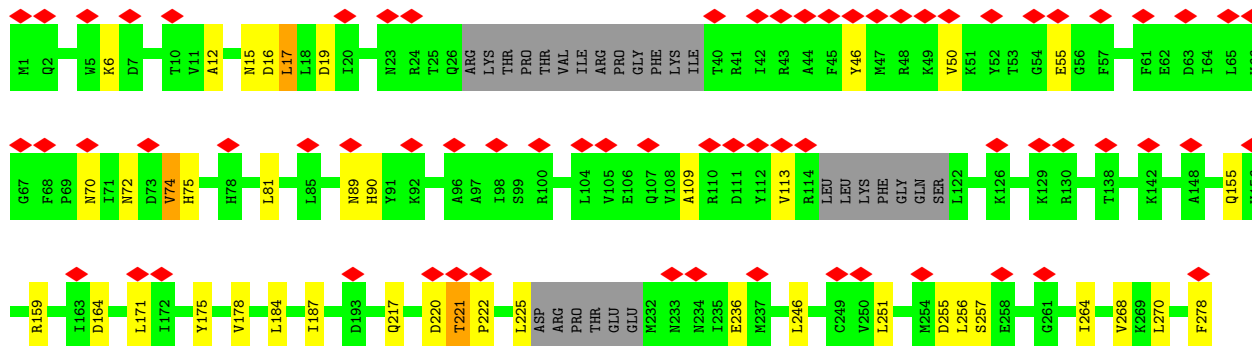
- Molecule 21: 60S ribosomal protein L26-A

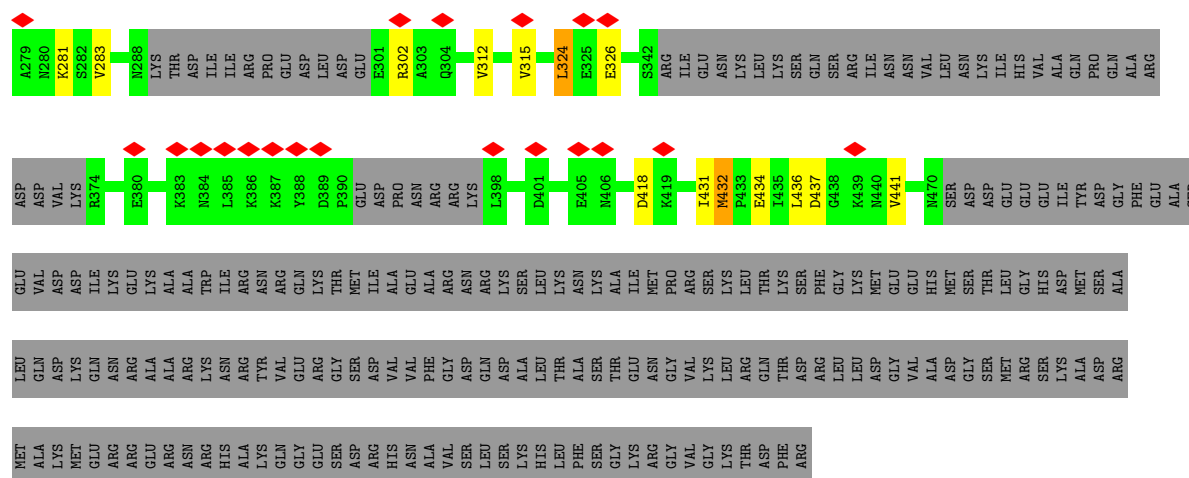
Chain Y: 88% 10%



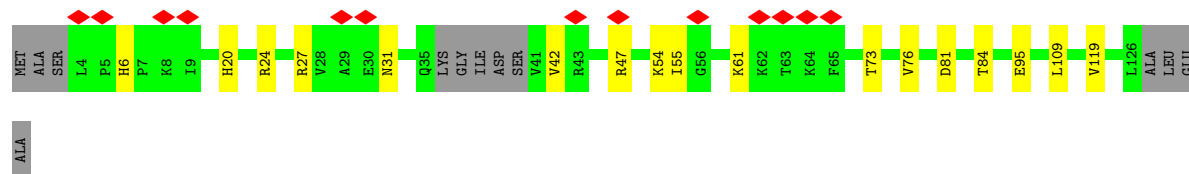
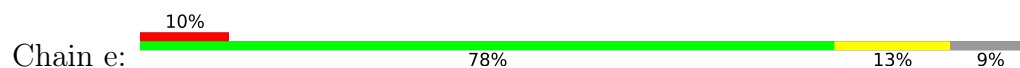
- Molecule 22: Nucleolar GTP-binding protein 1

Chain b: 14% 52% 8% 39%

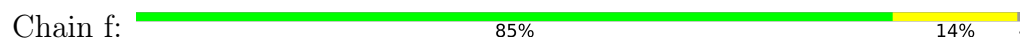




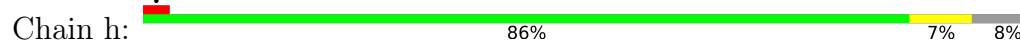
• Molecule 23: 60S ribosomal protein L32



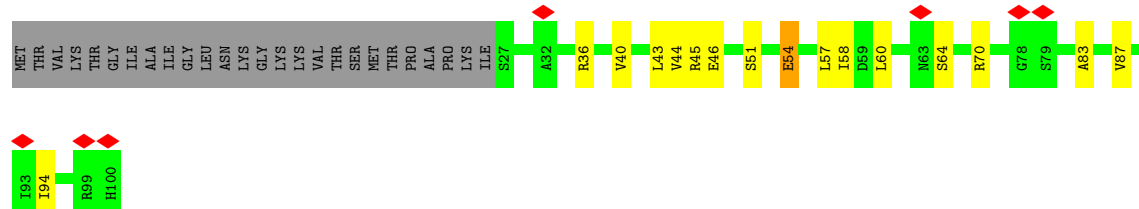
• Molecule 24: 60S ribosomal protein L33-A



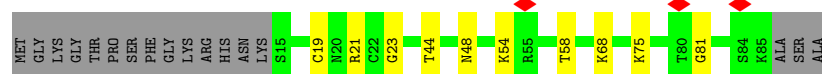
• Molecule 25: 60S ribosomal protein L35-A



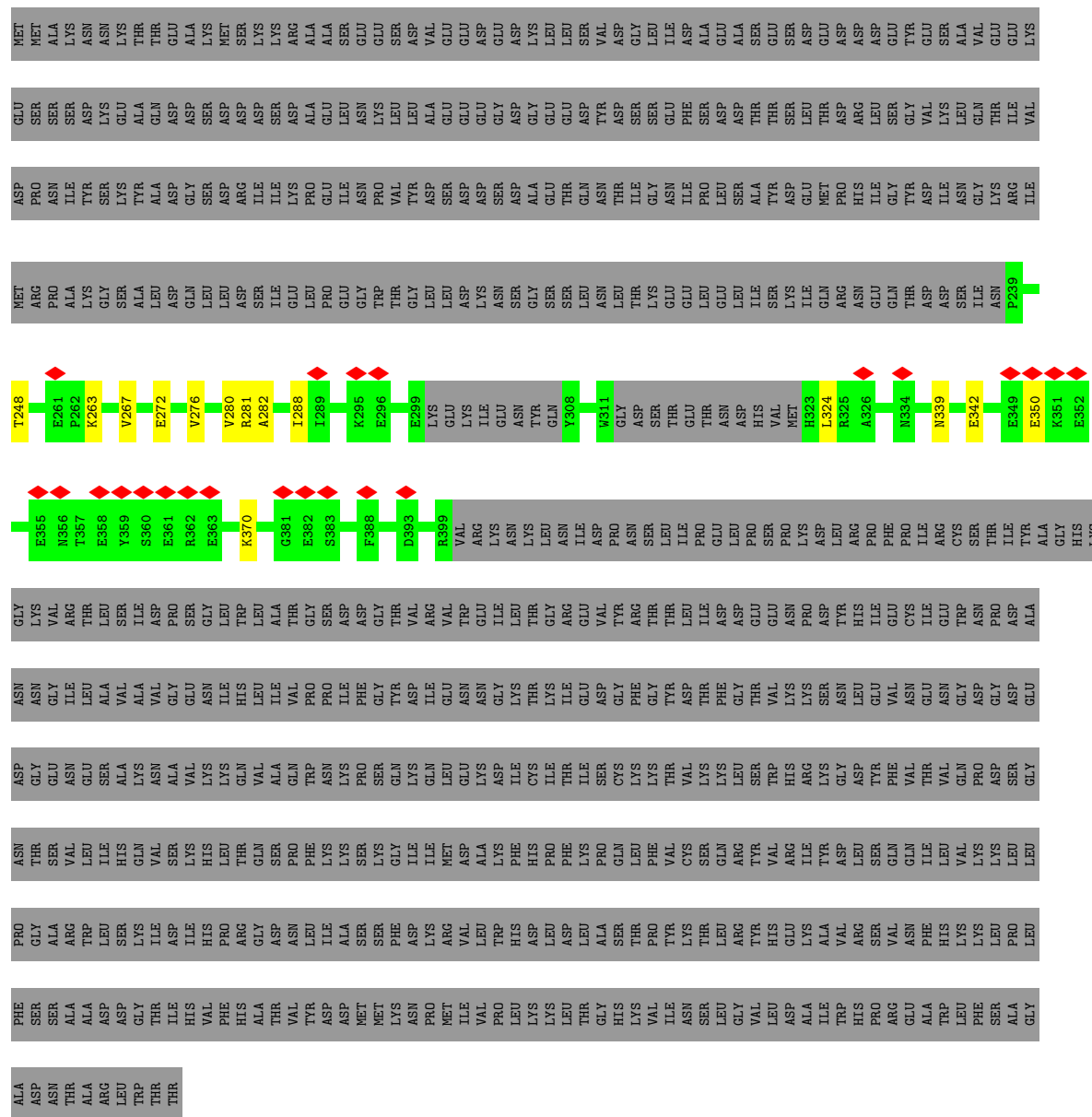
• Molecule 26: 60S ribosomal protein L36-A



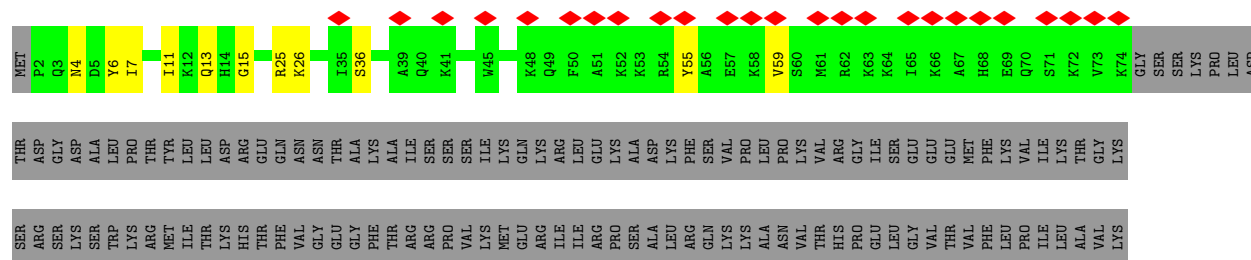
Chain j:



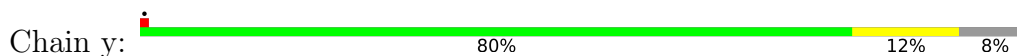
Chain m: 16% 82%



Chain n:



Chain t:



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	75514	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	86.09	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.087	Depositor
Minimum map value	-0.018	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.016	Depositor
Map size (Å)	425.40002, 425.40002, 425.40002	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0635, 1.0635, 1.0635	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section:
ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	1	0.08	0/37522	0.24	0/58404
2	2	0.08	0/3532	0.23	0/5494
3	6	0.09	0/1527	0.31	0/2371
4	B	0.11	0/2699	0.26	0/3626
5	C	0.09	0/2519	0.23	0/3409
6	D	0.13	0/1413	0.26	0/1896
7	E	0.10	0/1132	0.21	0/1518
8	F	0.10	0/1821	0.23	0/2451
9	G	0.10	0/1218	0.24	0/1648
10	H	0.08	0/1462	0.24	0/1969
11	K	0.09	0/1959	0.25	0/2642
12	L	0.13	0/877	0.30	0/1179
13	M	0.11	0/999	0.21	0/1344
14	N	0.12	0/1372	0.23	0/1836
15	O	0.10	0/1559	0.22	0/2091
16	P	0.10	0/769	0.21	0/1039
17	Q	0.11	0/973	0.23	0/1316
18	S	0.10	0/1413	0.24	0/1893
19	V	0.12	0/950	0.27	0/1279
20	W	0.10	0/1790	0.25	0/2410
21	Y	0.10	0/995	0.24	0/1329
22	b	0.09	0/3242	0.25	0/4368
23	e	0.10	0/981	0.22	0/1312
24	f	0.12	0/868	0.28	0/1168
25	h	0.11	0/912	0.25	0/1210
26	i	0.14	0/599	0.27	0/793
27	j	0.12	0/578	0.25	0/767
28	m	0.10	0/1242	0.24	0/1678
29	n	0.11	0/2642	0.25	0/3569
30	o	0.10	0/1000	0.23	0/1328
31	r	0.09	0/638	0.22	0/837
32	t	0.14	0/1813	0.32	0/2439

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	v	0.10	0/1043	0.22	0/1378
34	y	0.08	0/1722	0.23	0/2343
All	All	0.09	0/85781	0.25	0/124334

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	33556	16855	16900	396	0
2	2	3163	1601	1603	42	0
3	6	1370	691	692	25	0
4	B	2646	2728	2726	35	0
5	C	2474	2597	2593	25	0
6	D	1385	1384	1378	20	0
7	E	1116	1212	1210	10	0
8	F	1784	1863	1862	17	0
9	G	1198	1261	1258	23	0
10	H	1442	1513	1512	18	0
11	K	1928	2026	2022	26	0
12	L	864	918	917	17	0
13	M	984	1080	1079	5	0
14	N	1345	1388	1385	24	0
15	O	1531	1640	1638	5	0
16	P	757	767	764	12	0
17	Q	960	1040	1039	17	0
18	S	1380	1425	1423	12	0
19	V	936	987	986	14	0
20	W	1760	1787	1784	22	0
21	Y	984	1076	1075	10	0
22	b	3186	3221	3215	34	0
23	e	961	1029	1027	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	f	850	881	880	11	0
25	h	905	1006	1005	6	0
26	i	594	642	641	14	0
27	j	566	571	566	7	0
28	m	1207	1208	1206	11	0
29	n	2580	2642	2635	26	0
30	o	983	1026	1024	14	0
31	r	628	660	660	10	0
32	t	1789	1895	1892	24	0
33	v	1031	1077	1073	10	0
34	y	1701	1697	1697	20	0
35	j	1	0	0	0	0
All	All	80545	63394	63367	832	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

The worst 5 of 832 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1405:U:O2'	1:1:1406:A:OP1	1.73	1.06
1:1:3069:G:O2'	1:1:3070:A:O5'	1.83	0.95
1:1:1405:U:HO2'	1:1:1406:A:P	1.92	0.93
2:2:78:G:O2'	2:2:79:A:O5'	1.89	0.89
1:1:480:C:O4'	1:1:482:C:N4	2.06	0.89

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	B	329/387 (85%)	303 (92%)	25 (8%)	1 (0%)	36	69
5	C	312/362 (86%)	299 (96%)	13 (4%)	0	100	100
6	D	153/505 (30%)	140 (92%)	11 (7%)	2 (1%)	9	40
7	E	136/176 (77%)	132 (97%)	4 (3%)	0	100	100
8	F	220/244 (90%)	212 (96%)	8 (4%)	0	100	100
9	G	149/256 (58%)	138 (93%)	11 (7%)	0	100	100
10	H	177/191 (93%)	169 (96%)	8 (4%)	0	100	100
11	K	231/376 (61%)	216 (94%)	15 (6%)	0	100	100
12	L	106/199 (53%)	100 (94%)	5 (5%)	1 (1%)	14	47
13	M	124/138 (90%)	122 (98%)	2 (2%)	0	100	100
14	N	152/204 (74%)	150 (99%)	2 (1%)	0	100	100
15	O	190/199 (96%)	184 (97%)	6 (3%)	0	100	100
16	P	92/184 (50%)	92 (100%)	0	0	100	100
17	Q	123/186 (66%)	121 (98%)	2 (2%)	0	100	100
18	S	159/172 (92%)	151 (95%)	8 (5%)	0	100	100
19	V	124/137 (90%)	117 (94%)	7 (6%)	0	100	100
20	W	211/236 (89%)	206 (98%)	5 (2%)	0	100	100
21	Y	123/127 (97%)	118 (96%)	5 (4%)	0	100	100
22	b	380/647 (59%)	361 (95%)	17 (4%)	2 (0%)	24	59
23	e	114/130 (88%)	113 (99%)	1 (1%)	0	100	100
24	f	104/107 (97%)	99 (95%)	5 (5%)	0	100	100
25	h	107/120 (89%)	102 (95%)	5 (5%)	0	100	100
26	i	72/100 (72%)	68 (94%)	4 (6%)	0	100	100
27	j	69/88 (78%)	67 (97%)	2 (3%)	0	100	100
28	m	136/807 (17%)	126 (93%)	10 (7%)	0	100	100
29	n	300/605 (50%)	289 (96%)	11 (4%)	0	100	100
30	o	114/220 (52%)	108 (95%)	6 (5%)	0	100	100
31	r	71/261 (27%)	70 (99%)	1 (1%)	0	100	100
32	t	220/322 (68%)	207 (94%)	12 (6%)	1 (0%)	24	59
33	v	113/231 (49%)	110 (97%)	3 (3%)	0	100	100
34	y	223/245 (91%)	214 (96%)	8 (4%)	1 (0%)	30	64
All	All	5134/8162 (63%)	4904 (96%)	222 (4%)	8 (0%)	44	74

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	L	63	VAL
32	t	151	LEU
22	b	432	MET
4	B	342	LEU
22	b	6	LYS

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	B	280/323 (87%)	276 (99%)	4 (1%)	59	71
5	C	263/289 (91%)	260 (99%)	3 (1%)	65	74
6	D	154/440 (35%)	153 (99%)	1 (1%)	78	80
7	E	122/153 (80%)	121 (99%)	1 (1%)	73	77
8	F	186/205 (91%)	186 (100%)	0	100	100
9	G	125/208 (60%)	120 (96%)	5 (4%)	28	51
10	H	163/171 (95%)	162 (99%)	1 (1%)	78	80
11	K	220/346 (64%)	217 (99%)	3 (1%)	59	71
12	L	87/159 (55%)	84 (97%)	3 (3%)	32	55
13	M	99/109 (91%)	99 (100%)	0	100	100
14	N	136/176 (77%)	135 (99%)	1 (1%)	76	78
15	O	158/162 (98%)	154 (98%)	4 (2%)	42	62
16	P	80/146 (55%)	80 (100%)	0	100	100
17	Q	102/151 (68%)	101 (99%)	1 (1%)	68	75
18	S	148/156 (95%)	148 (100%)	0	100	100
19	V	98/105 (93%)	98 (100%)	0	100	100
20	W	196/213 (92%)	193 (98%)	3 (2%)	57	70
21	Y	108/110 (98%)	108 (100%)	0	100	100
22	b	352/573 (61%)	345 (98%)	7 (2%)	48	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	e	103/111 (93%)	103 (100%)	0	100	100
24	f	90/91 (99%)	90 (100%)	0	100	100
25	h	96/105 (91%)	96 (100%)	0	100	100
26	i	61/82 (74%)	59 (97%)	2 (3%)	33	56
27	j	59/71 (83%)	58 (98%)	1 (2%)	53	68
28	m	132/723 (18%)	132 (100%)	0	100	100
29	n	284/548 (52%)	279 (98%)	5 (2%)	51	67
30	o	105/199 (53%)	105 (100%)	0	100	100
31	r	65/229 (28%)	65 (100%)	0	100	100
32	t	200/287 (70%)	199 (100%)	1 (0%)	81	82
33	v	109/205 (53%)	109 (100%)	0	100	100
34	y	193/211 (92%)	193 (100%)	0	100	100
All	All	4574/7057 (65%)	4528 (99%)	46 (1%)	65	75

5 of 46 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
20	W	57	ARG
22	b	418	ASP
20	W	128	ASN
22	b	81	LEU
26	i	54	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 48 such sidechains are listed below:

Mol	Chain	Res	Type
22	b	208	HIS
24	f	88	ASN
22	b	259	GLN
23	e	35	GLN
27	j	76	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1530/3396 (45%)	320 (20%)	36 (2%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	2	146/158 (92%)	33 (22%)	1 (0%)
3	6	64/232 (27%)	23 (35%)	1 (1%)
All	All	1740/3786 (45%)	376 (21%)	38 (2%)

5 of 376 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	2	U
1	1	3	U
1	1	14	U
1	1	15	C
1	1	20	A

5 of 38 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	3151	U
1	1	3395	G
1	1	3153	U
1	1	3269	U
3	6	1	C

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

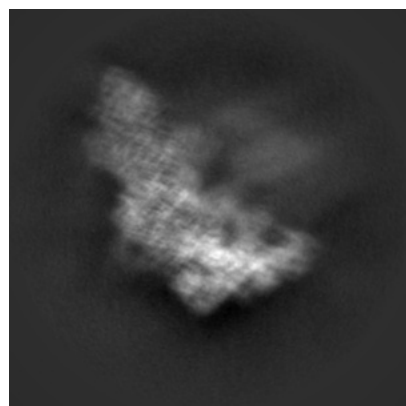
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12904. These allow visual inspection of the internal detail of the map and identification of artifacts.

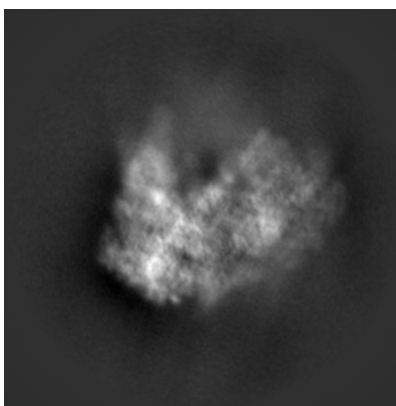
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

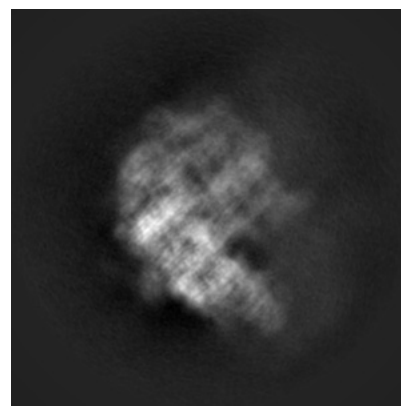
6.1.1 Primary map



X

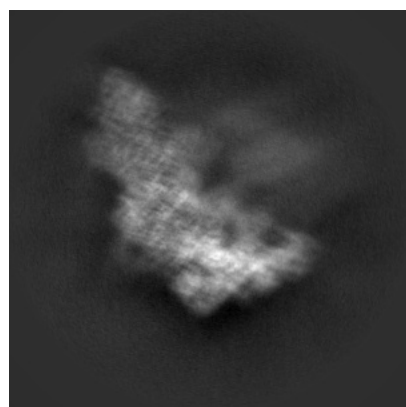


Y

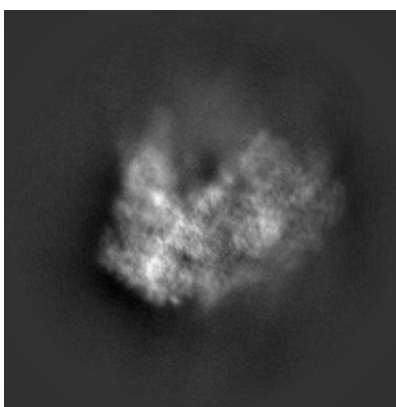


Z

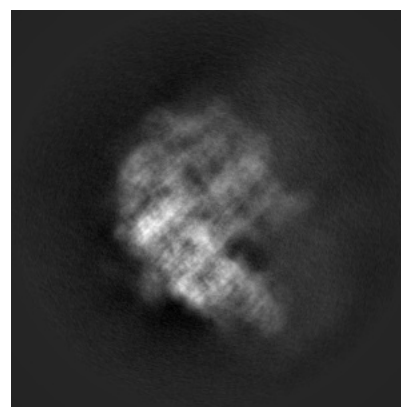
6.1.2 Raw map



X



Y

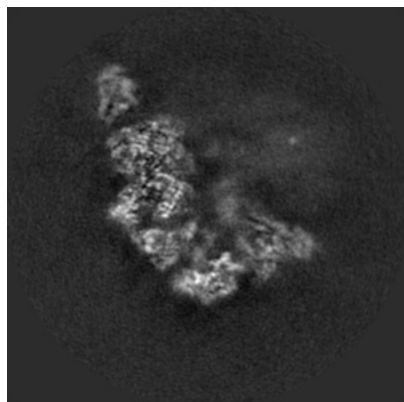


Z

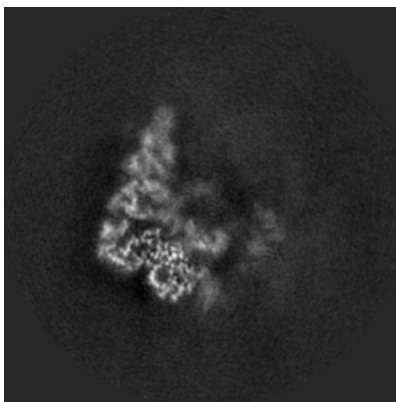
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

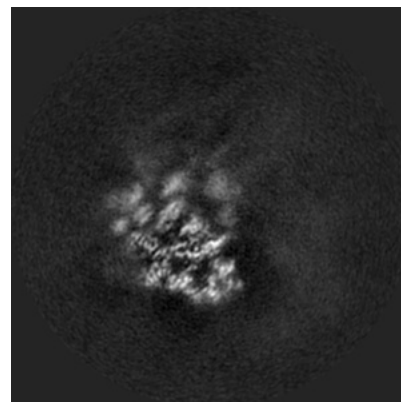
6.2.1 Primary map



X Index: 200

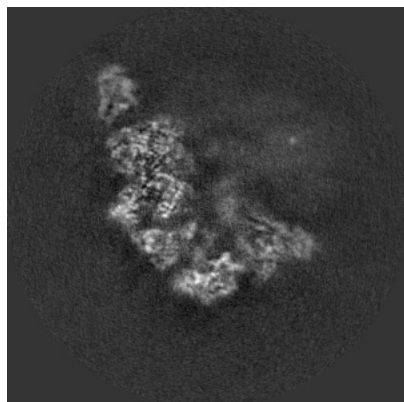


Y Index: 200

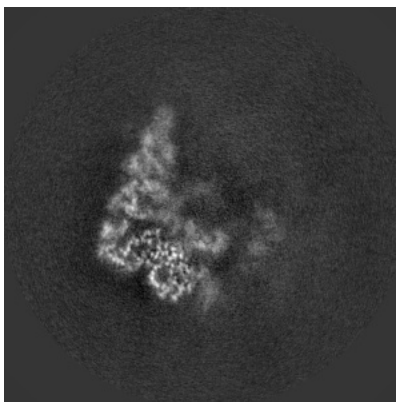


Z Index: 200

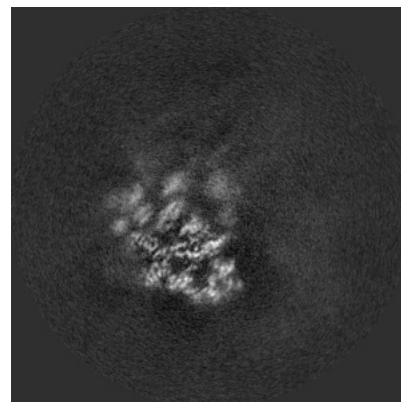
6.2.2 Raw map



X Index: 200



Y Index: 200

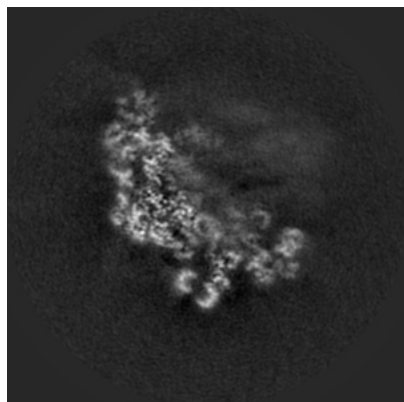


Z Index: 200

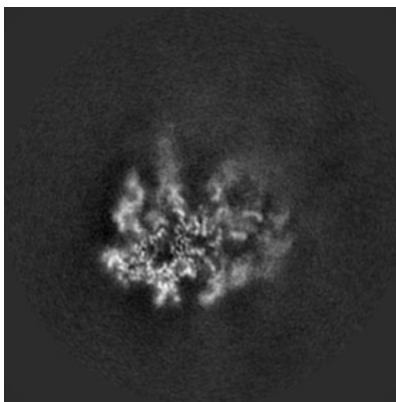
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

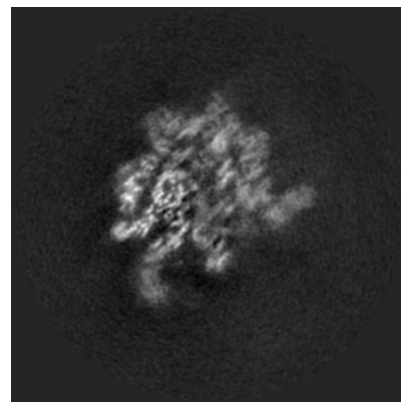
6.3.1 Primary map



X Index: 179

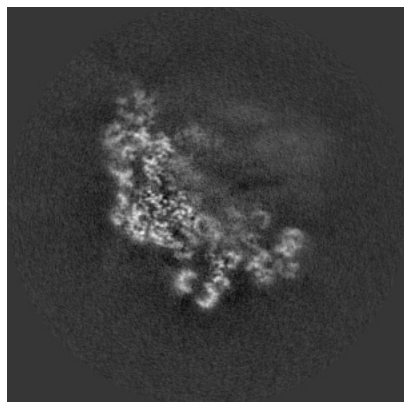


Y Index: 178

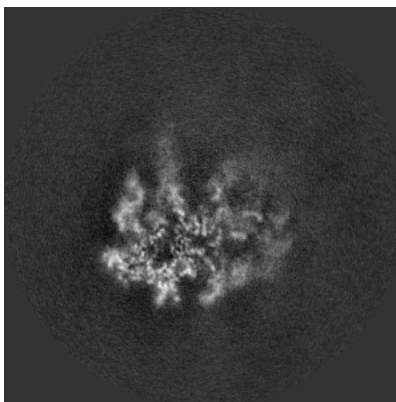


Z Index: 155

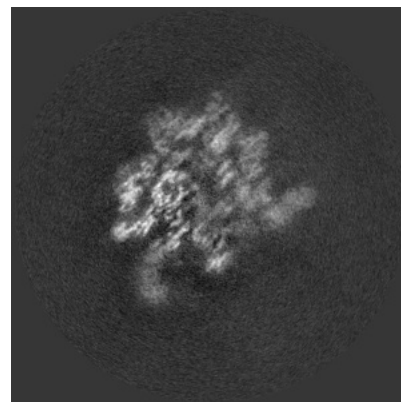
6.3.2 Raw map



X Index: 179



Y Index: 178

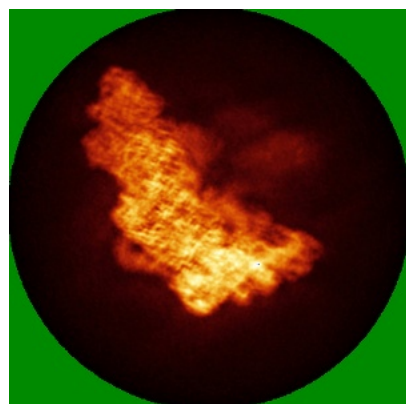


Z Index: 156

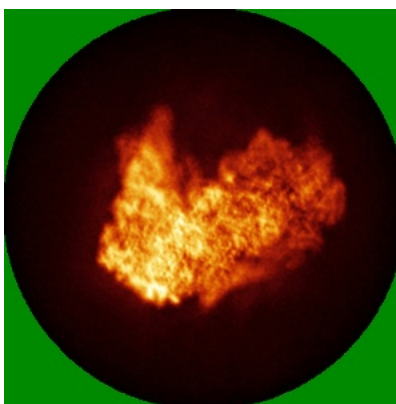
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

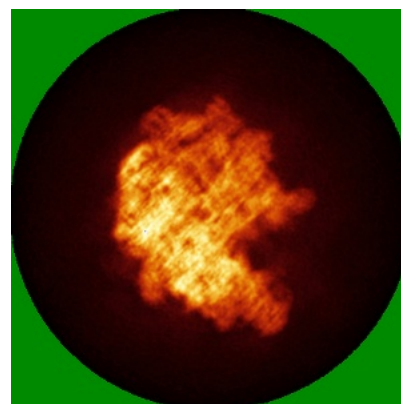
6.4.1 Primary map



X

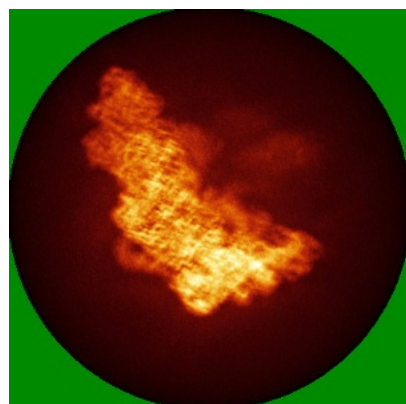


Y



Z

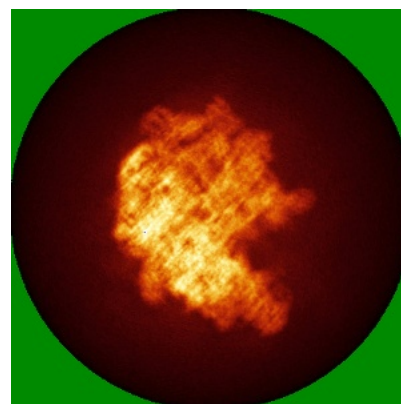
6.4.2 Raw map



X



Y

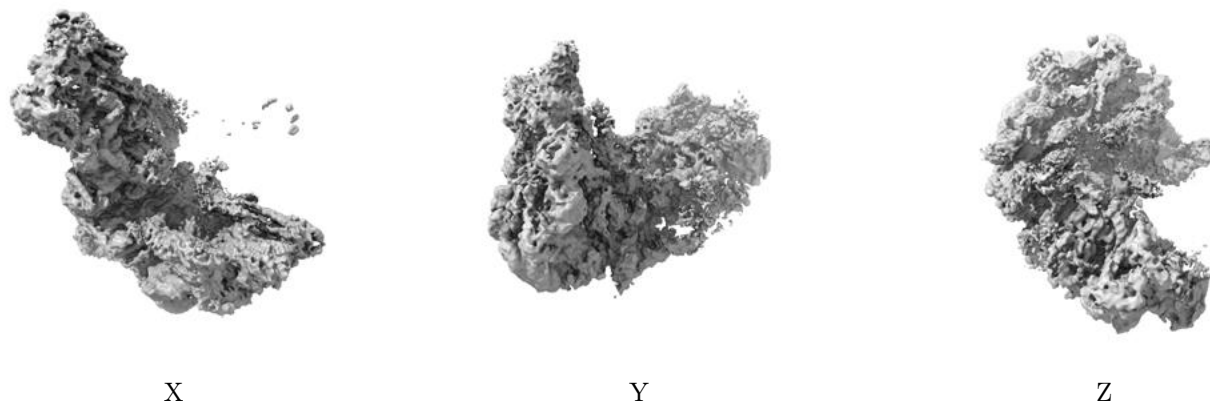


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

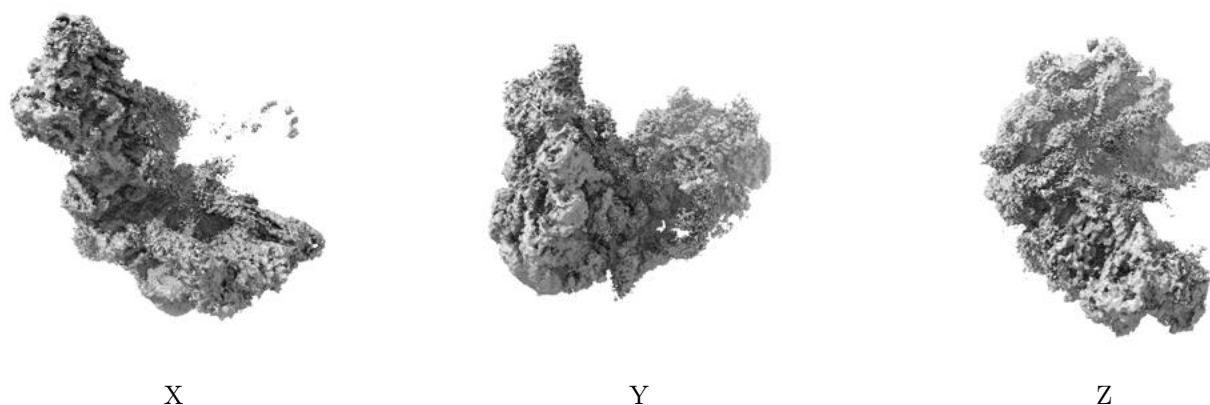
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.016. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

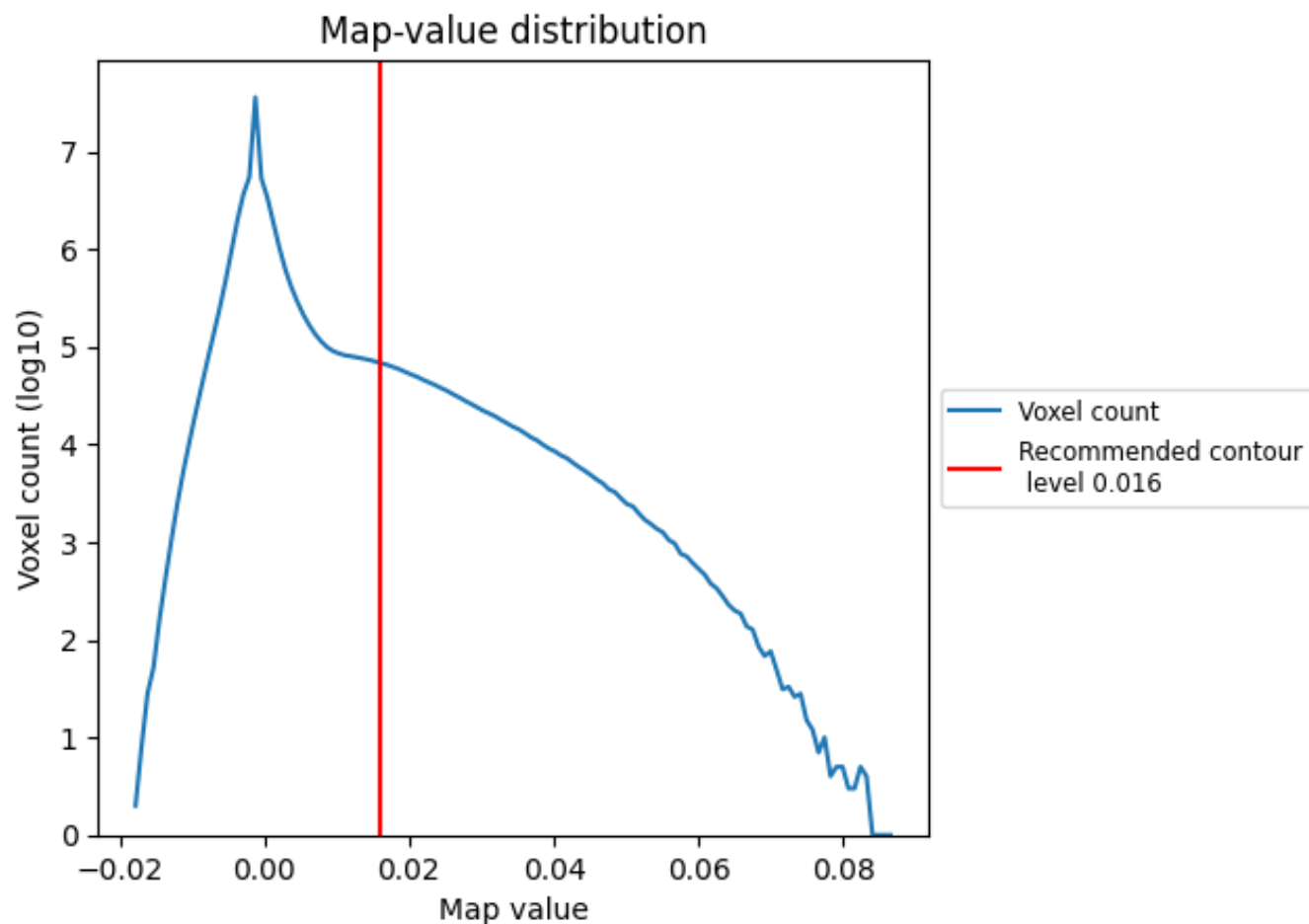
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

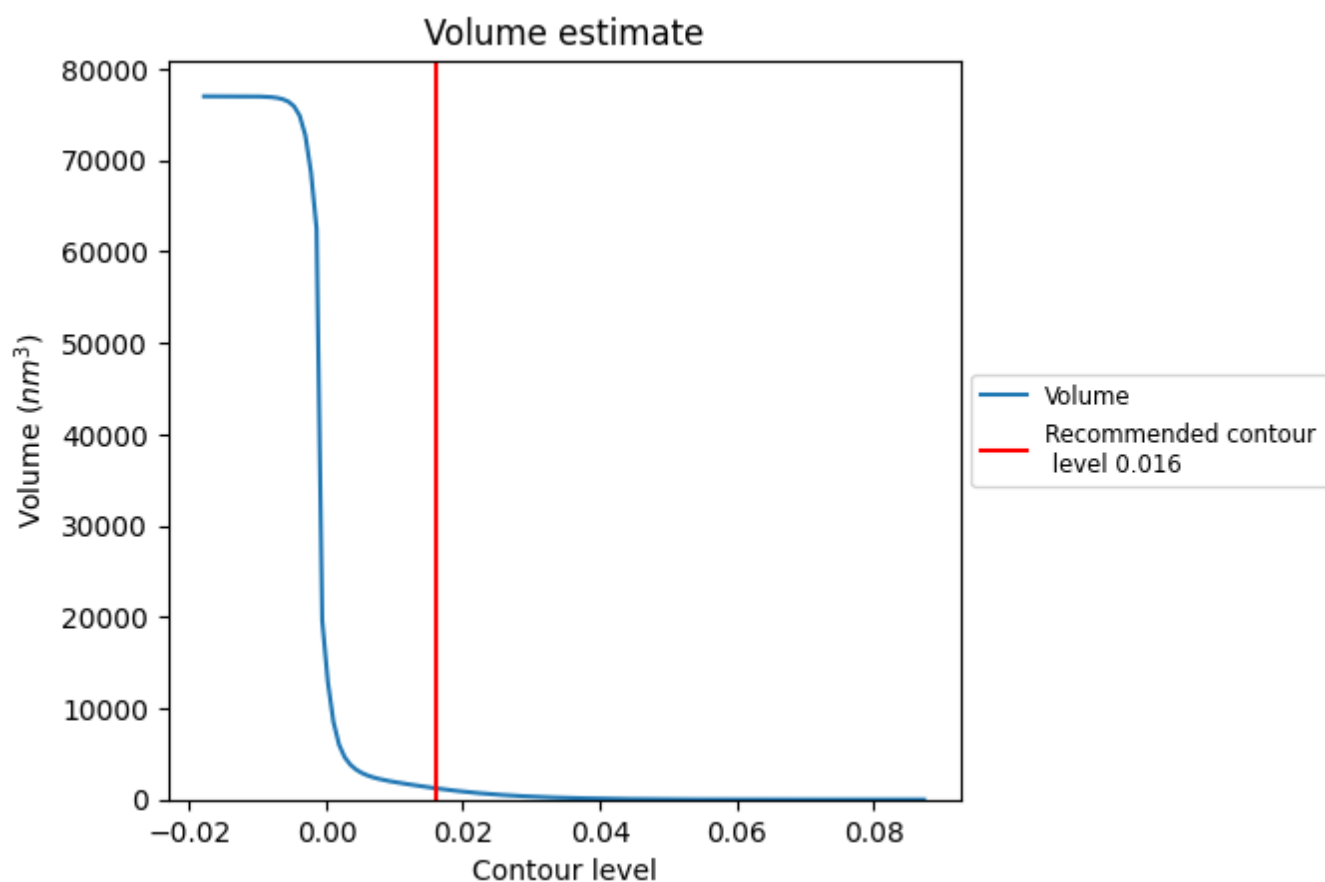
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

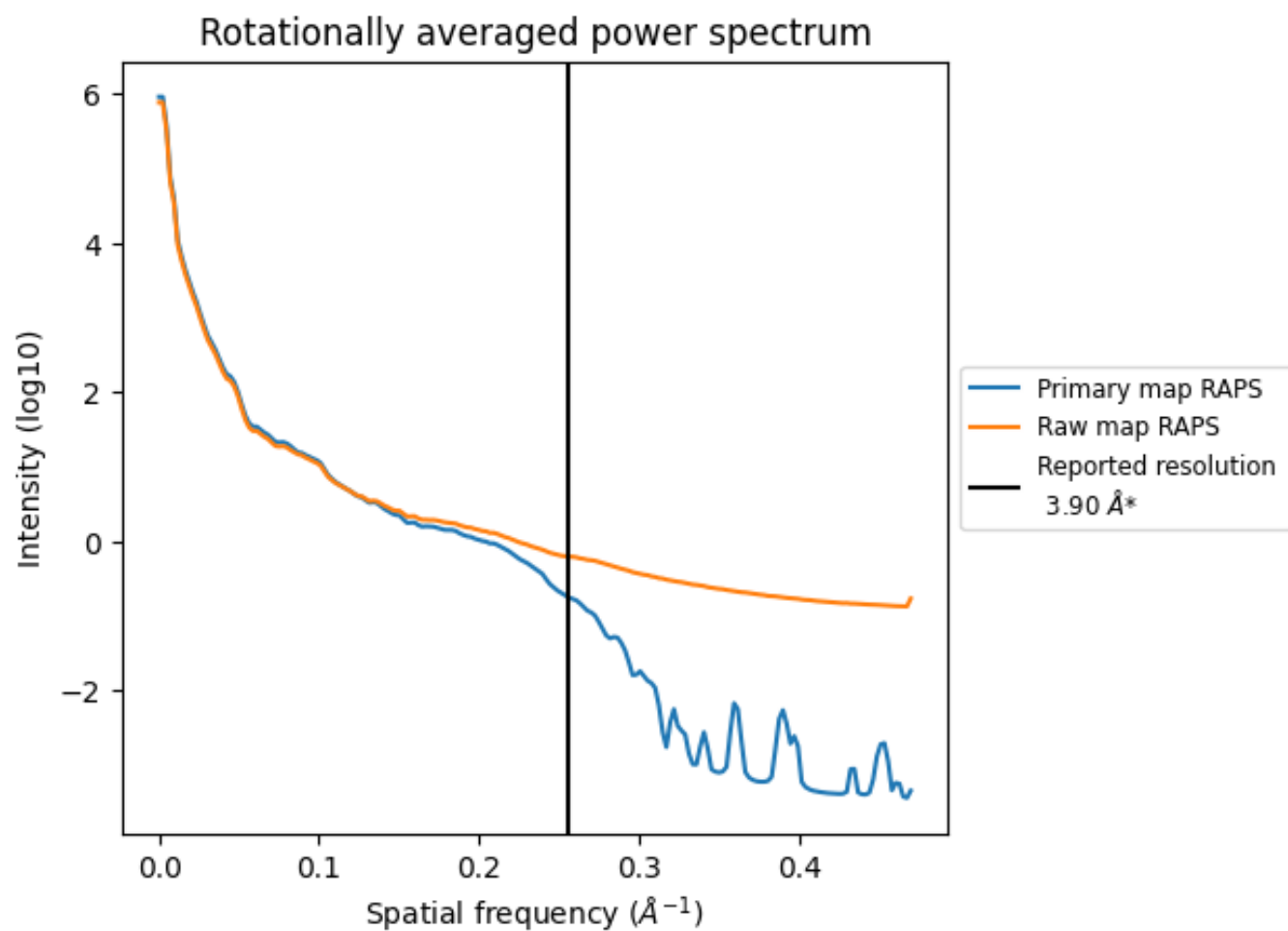
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1238 nm³; this corresponds to an approximate mass of 1118 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

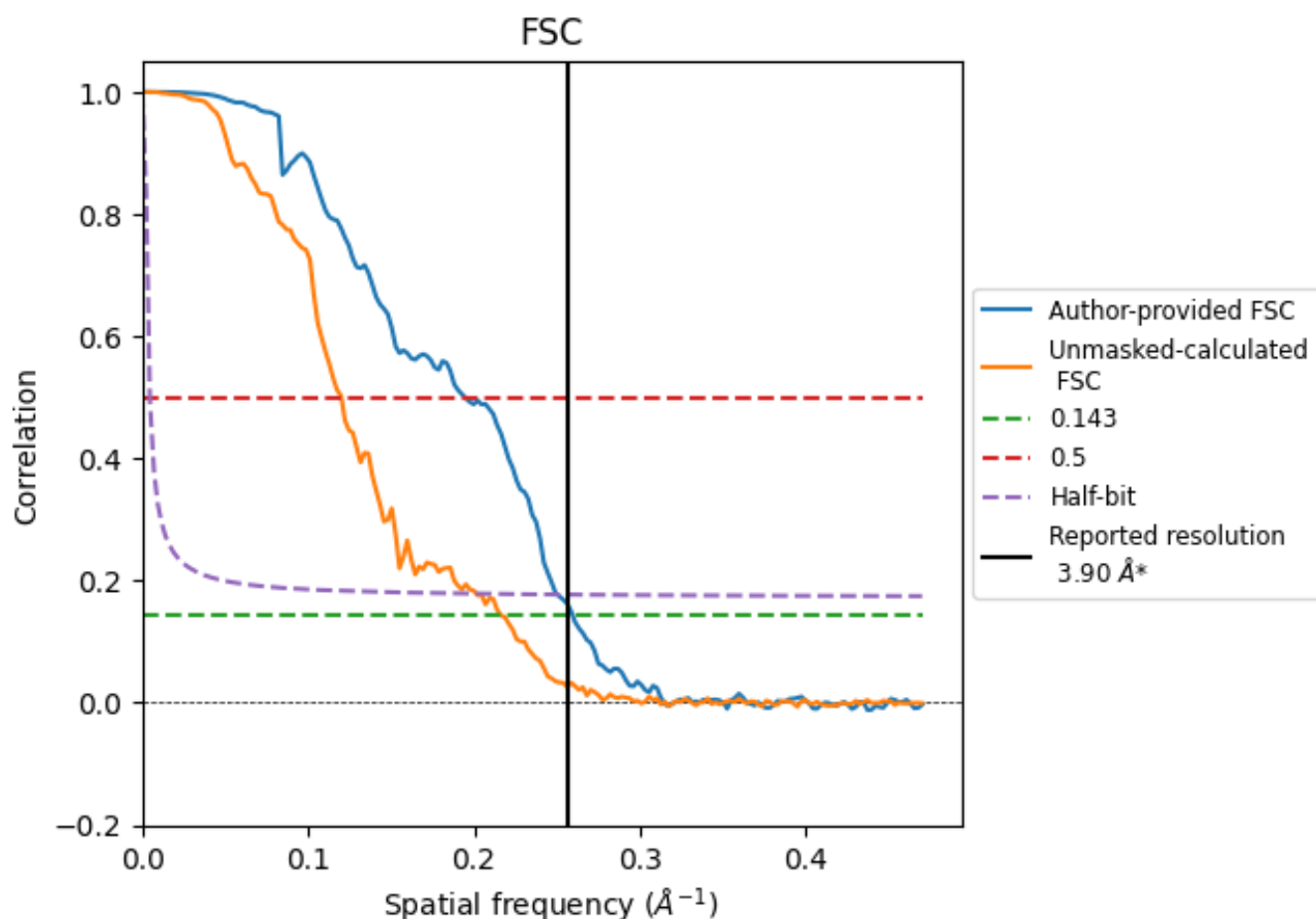


*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.256 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

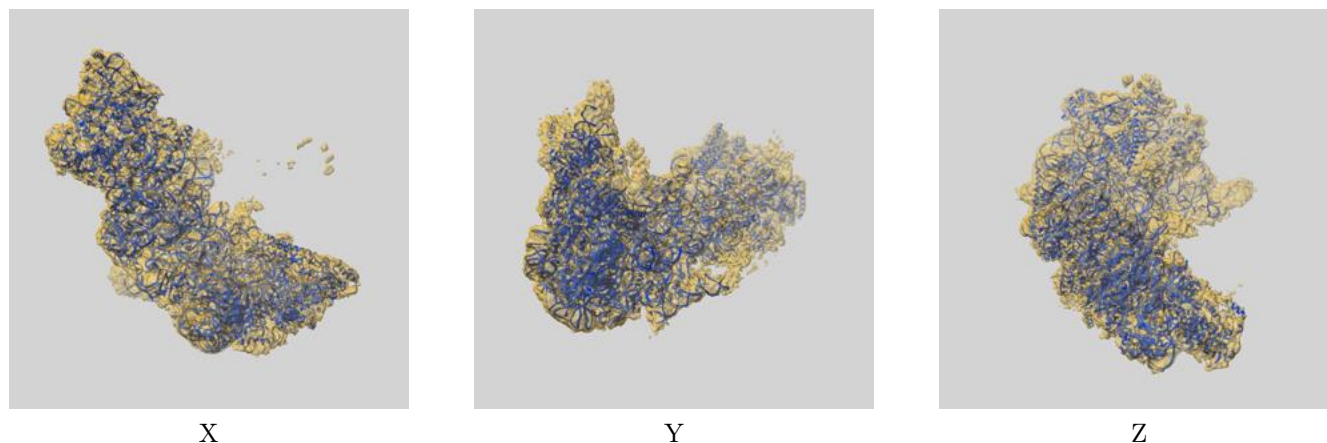
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	3.86	5.14	4.00
Unmasked-calculated*	4.63	8.33	4.97

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.63 differs from the reported value 3.9 by more than 10 %

9 Map-model fit [i](#)

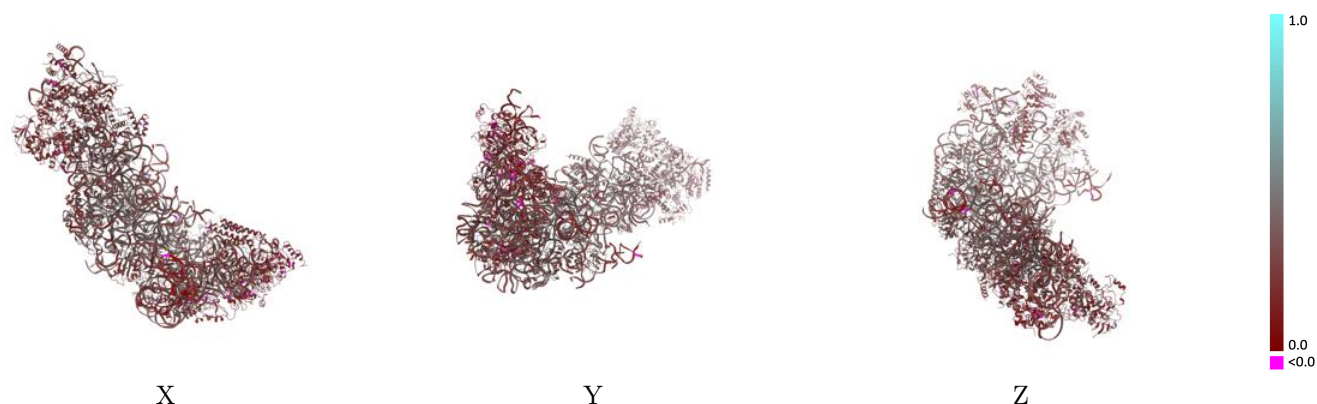
This section contains information regarding the fit between EMDB map EMD-12904 and PDB model 7OHP. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



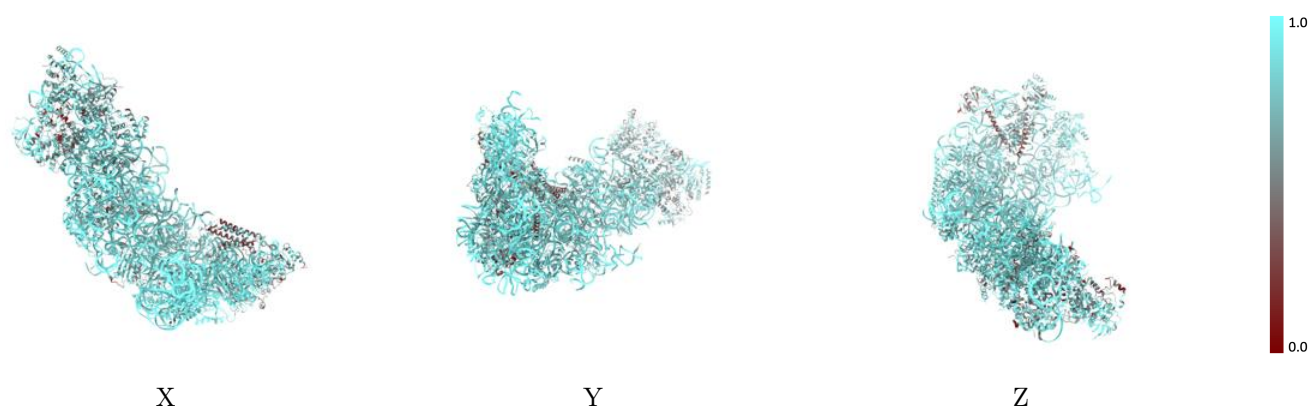
The images above show the 3D surface view of the map at the recommended contour level 0.016 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



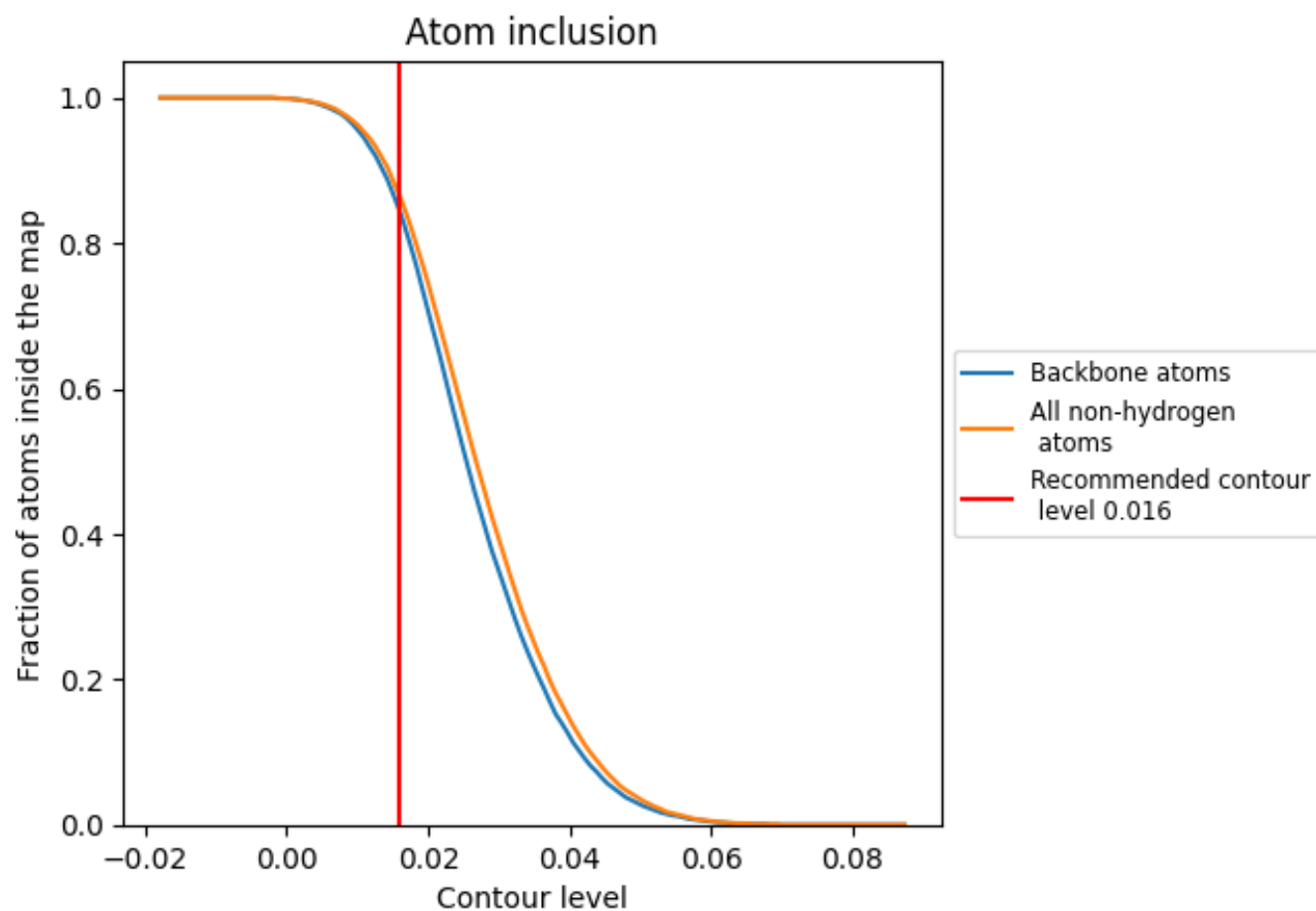
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.016).

9.4 Atom inclusion ⓘ



At the recommended contour level, 84% of all backbone atoms, 86% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.016) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8650	 0.2950
1	 0.9550	 0.2970
2	 0.9530	 0.3040
6	 0.8670	 0.2690
B	 0.9480	 0.2720
C	 0.8470	 0.3650
D	 0.6360	 0.2630
E	 0.9330	 0.3670
F	 0.8830	 0.3480
G	 0.7530	 0.3040
H	 0.7450	 0.3180
K	 0.6570	 0.2370
L	 0.8480	 0.3460
M	 0.8950	 0.3430
N	 0.7670	 0.3370
O	 0.8540	 0.3450
P	 0.7440	 0.2780
Q	 0.8090	 0.3460
S	 0.9040	 0.3330
V	 0.8370	 0.2450
W	 0.5570	 0.2290
Y	 0.8940	 0.3590
b	 0.6510	 0.2010
e	 0.6810	 0.3790
f	 0.8550	 0.3950
h	 0.7680	 0.3300
i	 0.7470	 0.2640
j	 0.8450	 0.3540
m	 0.6750	 0.2650
n	 0.7250	 0.2600
o	 0.6970	 0.2510
r	 0.5800	 0.2560
t	 0.6800	 0.2640
v	 0.7140	 0.3140
y	 0.9310	 0.2180

